In the Specification

On page 27, please amend the paragraph on lines 6-15 as follows:

--Figure 1. N18g0 RNA (SEQ ID NO:75) plus substrate showing construction of the size constrained random (N = 18) domain. The diversity of g0 was 4^{18} (6.9×10^{10}). The design is a bimolecular configuration analogous to that proposed by Haseloff and Gerlach (13), comprising two antisense regions separated by a metal dependent catalytic domain. Helix I and III were formed by association with a biotinylated RNA substrate (SEQ ID NO:76) (IL2bioS). Helix III is not shown in full. Notation on the random positions indicates correspondent nucleotide base identity and positions for the hammerhead (53). In the hammerhead, helix II is an extended RNA hairpin comprising 3 - 6 Watson-Crick base pairs. The Enzyme strand (E) promotes 2'-O mediated cleavage of the substrate strand (S) immediately 3' to C17 (indicated by arrow)--

On page 28, please amend the paragraph on lines 8-14 as follows:

--Figure 4. Sequence alignment showing composition of the N18 domain in the selected populations. Variable regions are highlighted. (a) Shows a sampling of the cloned fraction of the g4 population and indicates the state of enrichment after 4 rounds of low stringency selection. Linker positions are numbered 10.1, L.1-L.4, and 11.1 (SEQ ID NOS.:77-107) (b) The sampled fraction of the g6 populations showing the impact of high stringency selection on the identity of the variable (linker) region (positions 10.1-11.1 inclusive). (SEQ ID NOS.: 108-153)--